Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Original) A computer-implemented method of identifying whether a patient test sample is associated with one or more of a plurality of specific systemic autoimmune diseases (SADs) based on autoantibody levels present in the patient test sample; the method comprising:

storing a plurality of reference data sets in a memory, each data set having values representing levels for each of a plurality of specific autoantibodies, wherein said reference data sets include, for each of said specific SADs, at least one reference data set having an association with the specific SAD, and wherein said reference data sets include at least one reference data set associated with none of the specific SADs;

receiving a sample data set having values representing levels for each of said plurality of autoantibodies for a patient test sample; and

automatically applying a k-nearest neighbor process to the sample data set and the reference data sets to produce a statistically derived decision indicating whether the patient test sample is associated with none, one or more of said specific SADs.

2. (Original) The computer-implemented method of claim 1, wherein the SADs include two or more systemic autoimmune diseases selected from the group consisting of systemic lupus erythmatosus, scleroderma (SLE), Sjögren's syndrome (SS), polymyositis (PMYO), dermatomyositis (DMYO), CREST, and mixed connective tissue disease (MCTD).

3. (Original) The computer-implemented method of claim 1, wherein the SADs include two or more systemic autoimmune diseases selected from the group consisting of systemic lupus erythmatosus (SLE), scleroderma, Sjögren's syndrome (SS), myositis (MYO), polymyositis (PMYO), dermatomyositis (DMYO), CREST, connective tissue disease (CTD), fibromyalgia, osteroarthritis (OA), Reynaud's syndrome and Rheumatoid arthritis (RA).

4. (Original) The computer-implemented method of claim 1, wherein said plurality of autoantibodies comprises antibodies to at least ten of the following antigens:

SSA 60,
SSA 52,
SSB 48,
Sm BB',
Sm D1,
Sm,
SmRNP
RNP 68,
RNP A,
RNP C,
Fibrillarin,
Riboproteins P0, P1, and P2,
dsDNA,
Nucleosome,
Ku,
Centromere A,
Centromere B,
Scl-70,
Pm-Scl,
RNA-Polymerases 1, 2, and 3,
Th,
Jo-1,
Mi-2,
PL7,
PL12, and
SRP.

5. (Original) The computer-implemented method of claim 1, wherein said plurality of autoantibodies consists of antibodies to the following antigens:

SSA 60,
SSA 52,
SSB 48,
Sm,
SmRNP,
RNP 68,
RNP A,
Riboproteins P0, P1, and P2,
dsDNA,
Nucleosome,
Centromere B,
Scl-70, and
Jo-1.

6. (Original) The computer-implemented method of claim 1, further including generating a display output including said indication of whether the patient test sample is associated with none, one or more of the specific SADs.

7. (Original) The computer-implemented method of claim 6, wherein generating includes transmitting display output data to a remote computer system and rendering the display output on a display screen coupled with the remote computer system.

8. (Original) The computer-implemented method of claim 1, wherein receiving includes receiving the sample data set from an automated test system over a network connection.

9. (Original) The computer-implemented method of claim 8, wherein storing includes receiving the reference data sets from the automated test system over the network connection.

10. (Original) The computer-implemented method of claim 1, wherein storing includes receiving the reference data sets from one or more test sources.

11. (Original) The computer-implemented method of claim 1, wherein the k-nearest neighbor process includes determining, for each of the reference data sets, a concordance value between the sample data set and the reference data set, and comparing each concordance value to a threshold value, wherein only a first plurality of the reference data sets having a concordance value that exceeds the threshold value are used by the process.

12. (Original) The computer-implemented method of claim 11, wherein the k-nearest neighbor process further includes determining, for each of the reference data sets, a distance metric value between the sample data set and the reference data set.

13. (Original) The computer-implemented method of claim 11, wherein the process further includes:

determining whether the number of the first plurality of reference data sets exceeds a minimum cutoff value, and

if not, providing an indication that the patient test sample is associated with none of the specific SADs, and

if so, determining whether the patient test sample is associated with one or more of the specific SADs.

14. (Original) The computer-implemented method of claim 11, wherein the process further includes determining a disease concordance value for each of the first plurality of reference data sets.

15. (Original) The computer-implemented method of claim 14, wherein determining a disease concordance value includes:

for each SAD associated with the first plurality of reference data sets:

adding the number of the first plurality of reference data sets associated with that SAD and dividing by the total number of the first plurality of reference data sets to produce a disease concordance value for that SAD.

16. (Original) The computer-implemented method o f claim 15, further including comparing each disease concordance value with a first threshold value, and returning the SAD associated with the concordance value that exceeds the first threshold value.

17. (Original) The computer-implemented method of claim 16, further including comparing each disease concordance value with a second threshold value, and returning the SAD associated with the concordance value that exceeds the second threshold value.

18. (Original) A computer system configured to provide output data indicating whether a patient test sample is associated with one or more of a plurality of specific systemic autoimmune diseases (SADs) based on autoantibody levels present in the patient test sample; the system comprising:

storage means for storing a plurality of reference data sets, each data set having values representing levels for each of a plurality of specific autoantibodies, wherein said reference data sets include, for each of said specific SADs, at least one reference data set having an association with the specific SAD, and wherein said reference data sets include at least one reference data set associated with none of the specific SADs;

a means for receiving a sample data set having values representing levels for each of said plurality of autoantibodies for a patient test sample;

a means for processing the sample data set and the reference data sets using a k-nearest neighbor process to produce a statistically derived decision indicating whether the patient test sample is associated with none, one or more of said specific SADs; and

a means for providing output data including the statistically derived decision.

19. (Original) The system of claim 18, wherein the SADs include two or more systemic autoimmune diseases selected from the group consisting of systemic lupus erythmatosus (SLE), scleroderma, Sjögren's syndrome (SS), myositis (MYO), polymyositis (PMYO), dermatomyositis (DMYO), CREST, connective tissue disease (CTD), fibromyalgia, osteroarthritis (OA), Reynaud's syndrome and Rheumatoid arthritis (RA).

20. (Original) The system of claim 18, wherein said plurality of autoantibodies comprises antibodies to at least ten of the following antigens:

SSA 60,
SSA 52,
SSB 48,
Sm BB',
Sm D1,
Sm,
SmRNP,
RNP 68,
RNP A,
RNP C,
Fibrillarin,
Riboproteins P0, P1, and P2,
dsDNA,
Nucleosome,
Ku,
Centromere A,
Centromere B,

Scl-70,
Pm-Scl,
RNA-Polymerases 1, 2, and 3,
Th,
Jo-1,
Mi-2,
PL7,
PL12, and
SRP.

21. (Original) The system of claim 18, wherein said plurality of autoantibodies consists of antibodies to the following antigens:

SSA 60,
SSA 52,
SSB 48,
Sm,
SmRNP,
RNP 68,
RNP A,
Riboproteins P0, P1, and P2,
dsDNA,
Nucleosome,
Centromere B,
Scl-70, and
Jo-1.

22. (Original) The system of claim 18, wherein the means for providing the output data includes one of a monitor for displaying the output data, a printer for printing the output data and a communication interface device for providing the output data to a separate computer system.

23. (Original) The system of claim 18, wherein the means for receiving the sample data set includes one of an interface device configured to receive data from a remote automated test system, a manual input device, and a device configured to read data from a computer readable medium.

24. (Original) The system of claim 18, wherein the storage means includes one of a RAM, a ROM, a computer readable disk medium, a hard disk drive and a separate database system.

25. (Original) The system of claim 18, wherein the k-nearest neighbor process determines, for each of the reference data sets, a concordance value between the sample data set and the reference data set, and compares each concordance value to a threshold value, wherein only a first plurality of the reference data sets having a concordance value that exceeds the threshold value are used by the process.

26. (Original) The system of claim 25, wherein the k-nearest neighbor process further determines, for each of the reference data sets, a distance metric value between the sample data set and the reference data set.

27. (Original) The system of claim 25, wherein the k-nearest neighbor process further determines whether the number of the first plurality of reference data sets exceeds a minimum cutoff value, and

if not, provides an indication that the patient test sample is associated with none of the specific SADs, and

if so, determines whether the patient test sample is associated with one or more of the specific SADs.

28. (Original) The system of claim 25, wherein the k-nearest neighbor process further determines a disease concordance value for each of the first plurality of reference data sets.

29. (Original) The system of claim 28, wherein a disease concordance value is determined for each SAD associated with the first plurality of reference data sets by adding the number of the first plurality of reference data sets associated with that SAD and dividing by the total number of the first plurality of reference data sets to produce a disease concordance value for that SAD.

30. (Original) The system of claim 29, wherein the process further compares each disease concordance value with a first threshold value, and returns the SAD associated with the concordance value that exceeds the first threshold value.

31. (Original) The system of claim 30, wherein the process further compares each disease concordance value with a second threshold value, and returns the SAD associated with the concordance value that exceeds the second threshold value.